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APR 2 4 2002 97 A

TECH CENTER 1600/290

## SEQUENCE LISTING

Hall, Roderick L. Poll, Christopher T. Newton, Benjamin B. Taylor, William J.A.

<120> Method For Accelerating The Rate of Mucociliary Clearance

<130> 98-736

<140> US 09/218,913 <141> 1998-12-22

<160> 105

<170> PatentIn version 3.1

<210> 1

<211> 179

<212> PRT

<213> Homo sapiens

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Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr 20 25 30

Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser 35 40 45

Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val 50 60

Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp 65 70 75 80

Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser 85 90 95

Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr 100 105 110

Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg 115 120 125 Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn 130 135 140

and the second of the second o

Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln 145 150 155 160

Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Leu Ala Gly 165 170 175

Ala Val Ser

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<211> 197

<212> PRT

<213> Homo sapiens

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Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser 20 25 30

Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn 35 40 45

Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly 50 55 60

Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala 65 70 75 80

Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala 85 90 95

Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp 100 105 110 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala 115 120 125

Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val 130 135 140

Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn 145 150 155 160

Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg 165 170 175

Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Leu 180 185 190

Ala Gly Ala Val Ser 195

<210> 3

<211> 153

<212> PRT

<213> Homo sapiens

<400> 3

Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala 1 5 10 15

Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu 20 25 30

Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys 35 40 45

Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly 50 55 60

Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala 65 70 75 80

Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr 85 90 95

Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser 100 105 110 Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe 115 120 125

Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu 130 135 140

Ala Cys Met Leu Arg Cys Phe Arg Gln 145 150

<210> 4

<211> 58

<212> PRT

<213> Homo sapiens

<400> 4

Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala 1 5 10 15

Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu  $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys 35 40 45

Glu Glu Cys Leu Lys Lys Cys Ala Thr Val 50

<210> 5

<211> 51

<212> PRT

<213> Homo sapiens

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Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly
20 25 30

Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu  $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$ 

Lys Lys Cys

50

<210> 6

<211> 58

<212> PRT

<213> Homo sapiens

<400> 6

Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala 1 5 10 15

Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn 20 25 30

Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu 35 40 45

Glu Ala Cys Met Leu Arg Cys Phe Arg Gln 50 55

<210> 7

<211> 51

<212> PRT

<213> Homo sapiens

<400> 7

Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg 1 5 10 15

Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly 20 25 30

Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met 35 40 45

Leu Arg Cys 50

<210> 8

<211> 92

<212> PRT

<213> Homo sapiens

<400> 8

Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val

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Val Gly Arg Cys		Pro Arg Trp Trp Tyr	Asn Val Thr 30
Asp Gly Ser Cys 35	Gln Leu Phe Val 1 40	Yr Gly Gly Cys Asp 45	Gly Asn Ser
Asn Asn Tyr Leu 50	Thr Lys Glu Glu (	ys Leu Lys Lys Cys 60	Ala Thr Val
Thr Glu Asn Ala	Thr Gly Asp Leu A	la Thr Ser Arg Asn 75	Ala Ala Asp 80
Ser Ser Val Pro	Ser Ala Pro Arg A	arg Gln Asp Ser 90	
	al Sequence		
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<220> <221> misc_fea <222> (707)( <223> "n" is a	707)		
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ctccatgcct aggt	ggtggt acaatgtcac	tgacggatcc tgccagct	gt ttgtgtatgg 180
gggctgtgac ggaa	acagca ataattacct	gaccaaggag gagtgcct	ca agaaatgtgc 240
cactgtcaca gaga	atgcca cgggtgacct	ggccaccagc aggaatgc	ag cggattcctc 300
tgtcccaagt gctc	ccagaa ggcaggattc	tgàagaccac tccagcga	ta tgttcaacta 360
tgaagaatac tgca	ccgcca acgcagtcac	tgggccttgc cgtgcatc	ct tcccacgctg 420

gtactttgac	gtggagagga	actcctgcaa	taacttcatc	tatggaggct	gccggggcaa	480
taagaacagc	taccgctctg	aggaggcctg	catgctccgc	tgcttccgcc	agcaggagaa	540
tcctcccctg	ccccttggct	caaaggtggt	ggttctggcc	ggggctgttt	cgtgatggtg	600
ttgatccttt	tcctggggag	catccatggt	cttactgatt	ccgggtggca	aggaggaacc	660
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<210> 10

<211> 197

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acids -18 to 179 of translation of consensus sequence in Fig. 3.

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Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Ser Gly Val 1 5 10 15

Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser 20 25 30

Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn 35 40 45

Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly 50 55 60

Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala 70 75 80

Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala 85 90 95

Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
100 105 110

His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala 115 120 125

Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val 130 135 140

Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn 145 150 155 160

Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg 165 170 175

Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Leu 180 185 190

Ala Gly Ala Val Ser 195

<210> 11

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Variants of human Bikunin.

<220>

<221> MISC\_FEATURE

<222> (8)..(8)

<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

<221> MISC\_FEATURE

<222> (17)..(17)

<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

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<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

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<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa"

in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

- <220>
- <221> MISC\_FEATURE
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- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).
- <220>
- <221> MISC\_FEATURE
- <222> (42)..(42)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).
- <220>
- <221> MISC\_FEATURE
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- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).
- <220>
- <221> MISC\_FEATURE
- <222> (52)..(52)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).
- <220>
- <221> MISC\_FEATURE
- <222> (64)..(64)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).
- <220>
- <221> MISC\_FEATURE
- <222> (103)..(103)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

- <221> MISC\_FEATURE
- <222> (112)..(112)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

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<220>

- <221> MISC\_FEATURE
- <222> (114)..(114)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

- <221> MISC\_FEATURE
- <222> (116)..(121)
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<220>

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- <222> (135)..(135)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

- <221> MISC\_FEATURE
- <222> (137)..(137)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

- <221> MISC\_FEATURE
- <222> (140)..(142)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

<221> MISC\_FEATURE

- <222> (147)..(147)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

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- <220>
- <221> MISC\_FEATURE
- <222> (159)..(159)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

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- Ala Asp Arg Glu Arg Ser Ile Xaa Asp Phe Cys Leu Val Ser Lys Val 1 5 10 15
- Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Trp Trp Tyr Asn Val Thr
  20 25 30
- Asp Gly Ser Cys Gln Leu Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Ser 35 40 45
- Asn Asn Tyr Xaa Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Xaa 50 60
- Thr Glu Asn Ala Thr Gly Asp Leu Ser Thr Ser Arg Asn Ala Ala Asp 65 70 75 80
- Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu His Asp Ser 85 90 95
- Ser Asp Met Phe Asn Tyr Xaa Glu Tyr Cys Thr Ala Asn Ala Val Xaa 100 105 110
- Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Trp Tyr Phe Asp Val Glu Arg
- Asn Ser Cys Asn Asn Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Lys Asn 130 135 140
- Ser Tyr Xaa Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Xaa Gln 145 150 155 160

## Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly 165 170 175

## Ala Val Ser

<212> PRT

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	(36'	c_feature 7)(367) is any nuc:	leotide.				
	(384	c_feature 4)(384) is any nuc	leotide.				·
<220><221><222><223>	(39)	c_feature 0)(390) is any nucl	leotide.				
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accgaga	aacg	cagcatccac	gacttctgcc	tggtgtcgaa	ggtggtgggc	agattccggg	120
cctccat	tgcc	taggtggtgg	tacaatgtca	ctgacggatc	ctgccagctg	tttgtgtatg	180
ggggctg	gtga	cggaaacagc	aataattacc	tgaccaagga	ggagtgcctc	aagaaatgtg	240
ccactgt	ccac	agagaatgcc	acgggtgacc	tggccaccag	caggaatgca	gcggattcct	300
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Trp Pro Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
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                               25
Lys Val Val Gly Arg Glu Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
                           40
Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
    50
                       55
Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
                   70
65
                                       75
Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser
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<211> 510
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<213> Homo sapiens

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<223> "n" is any nucleotide.
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agaacgcagc atccacgact tctgcctggt gtcgaaggtg gtgggcagat gccgggcctc
                                                                     120
catgcctagg tggtggtaca atgtcactga cggatcctgc cagctgtttg tgtatggggg
                                                                     180
ctgtgacgga aacagcaata attacctgac caaggaggag tgcctcaaga aatgtgccac
                                                                     240
tgtcacagag aatgccacgg gtgacctggc caccagcagg aatgcagcgg attcctctgt
                                                                     300
cccaagtgct cccagaaggc aggattctga agaccactcc agcgatatgt tcaactatga
                                                                     360
agaatactgg caccgccaac gcattcactg ggcctgcgtg catccttccc acgctggtac
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tttgncg
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THE PARTY OF THE

20 Lys Tyr Gly Gly Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly 55 <210> 20 <211> 57 <212> PRT <213> Unknown <220> <223> Kunitz-like domain of tissue factor pathway inhibitor precursor. <400> 20 Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn 5 10 Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln

Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe

Glu Cys Leu Arg Ala Cys Lys Lys Gly 50 55

<210> 21 <211> 57 <212> PRT <213> Unknown

<220>
<223> Kunitz-like domain of tissue factor pathway inhibitor precursor 2.
<400> 21

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Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu 1 5 10 15

Leu Leu Arg Tyr Tyr Tyr Arg Tyr Arg Thr Gln Ser Cys Arg Gln Phe 20 25 30

Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu 40 Ala Cys Asp Asp Ala Cys Trp Arg Ile <210> 22 <211> 57 <212> PRT <213> Unknown <220> <223> Kunitz-like domain of tissue factor pathway inhibitor precursor 2. <400> 22 Pro Ser Phe Cys Tyr Ser Pro Lys Asp Glu Gly Leu Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe Asn Pro Arg Tyr Arg Thr Cys Asp Ala Phe 25 20 Thr Tyr Thr Gly Cys Gly Asn Asn Asn Asn Phe Val Ser Arg Glu 35 40 Asp Ser Lys Arg Ala Cys Ala Lys Ala 50 55 <210> 23 <211> 57 <212> PRT <213> Unknown <220> <223> Kunitz-like domain of amyloid precursor protein homologue. <400> 23 Lys Ala Val Cys Ser Gln Glu Ala Met Thr Gly Pro Cys Arg Ala Val Met Pro Arg Thr Thr Phe Asp Leu Ser Lys Gly Lys Cys Val Arg Phe 20

now the confidence with the

45

Ile Thr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Glu Ser Glu Asp

```
Tyr Cys Met Ala Val Cys Lys Ala Met
    50
<210> 24
<211> 58
<212> PRT
<213> Unknown
<220>
<223> Kunitz-like domain of aprotinin.
<400> 24
Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Lys Ala
Arg Ile Ile Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
                                25
Phe Val Tyr Gly Gly Cys Arg Ala Lys Arg Asn Asn Phe Lys Ser Ala
Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
<210> 25
<211> 51
<212> PRT
<213> Unknown
<220>
<223> Kunitz-like domain of inter-alpha-trypsin inhibitor precursor.
<400> 25
Cys Gln Leu Gly Tyr Ser Ala Gly Pro Cys Met Gly Met Thr Ser Arg
Tyr Phe Tyr Asn Gly Thr Ser Met Ala Cys Glu Thr Phe Gln Tyr Gly
            20
Gly Cys Met Gly Asn Gly Asn Asn Phe Val Thr Glu Lys Glu Cys Leu
Gln Thr Cys
    50
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<210> 26

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<211> 57
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<212> PRT

<213> Unknown

<220>

<223> Kunitz-like domain of inter-alpha-trypsin inhibitor precursor.

<400> 26

Val Ala Ala Cys Asn Leu Pro Ile Val Arg Gly Pro Cys Arg Ala Phe 1 5 10 15

Ile Gln Leu Trp Ala Phe Asp Ala Val Lys Gly Lys Cys Val Leu Phe 20 25 30

Pro Tyr Gly Gly Cys Gln Gly Asn Gly Asn Lys Phe Tyr Ser Glu Lys 35 40 45

Glu Cys Arg Glu Tyr Cys Gly Val Pro 50 55

<210> 27

<211> 57

<212> PRT

<213> Unknown

<220>

<223> Kunitz-like domain of amyloid precursor protein.

<400> 27

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Ile Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe 20 25 30

Phe Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu 35 40 45

Tyr Cys Met Ala Val Cys Gly Ser Ala 50 55

<210> 28

<211> 51

<212> PRT

<213> Unknown

<220>

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<223> Kunitz-like domain of collagen alpha-3(VI) precursor.
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Trp Tyr Tyr Asp Pro Asn Thr Lys Ser Cys Ala Arg Phe Trp Tyr Gly
Gly Cys Gly Gly Asn Glu Asn Lys Phe Gly Ser Gln Lys Glu Cys Glu
                            40
Lys Val Cys
    50
<210> 29
<211> ·57
<212> PRT
<213> Unknown
<220>
<223> Kunitz-like domain of HKI-B9.
<400> 29
Pro Asn Val Cys Ala Phe Pro Met Glu Lys Gly Pro Cys Gln Thr Tyr
Met Thr Arg Trp Phe Phe Asn Phe Glu Thr Gly Glu Cys Glu Leu Phe
            20
                                25
Ala Tyr Gly Gly Cys Gly Gly Asn Ser Asn Asn Phe Leu Arg Lys Glu
        35
                            40
Lys Cys Glu Lys Phe Cys Lys Phe Thr
    50
<210> 30
<211> 46
<212> DNA
<213> Artificial Sequence
<223> 5' sense oligonucleotide used in Example 6.
```

gccaagcttg gataaaagat atgaagaata ctgcaccgcc aacgca

46

```
<210> 31
<211>
      35
<212>
      DNA
<213> Artificial Sequence
<220>
<223>
      3' antisense oligonucleotide used in Example 6.
<400> 31
                                                                      35
ggggatcctc actgctggcg gaagcagcgg agcat
<210>
      32
<211>
      206
<212>
      DNA
<213> Artificial Sequence
<220>
<223> Cloned bikunin cDNA fragment in Example 6.
<400> 32
ccaagcttgg ataaaagata tgaagaatac tgcaccgcca acgcagtcac tgggccttgc
                                                                      60
cgtgcatcct tcccacgctg gtactttgac gtggagagga actcctgcaa taacttcatc
                                                                     120
tatggaggct gccggggcaa taagaacagc taccgctctg aggaggcctg catgctccgc
                                                                     180
tgcttccgcc agcagtgagg atcccc
                                                                     206
<210> 33
<211> 28
<212> DNA
<213> Artificial Sequence
<220>
<223>
      3' PCR primer used to amplify EST R74593.
<400> 33
                                                                      28
cgaagcttca tctccgaagc tccagacg
<210>
      34
<211>
      31
<212> DNA
<213> Artificial Sequence
<220>
<223>
      5' PCR primer used to amplify EST R74593.
<400> 34
                                                                      31
aggatctaga caataattac ctgaccaagg a
<210> 35
<211> 37
```

A DOMESTIC OF THE PARTY OF THE

```
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' PCR primer used to amplify EST R35464.
<400> 35
ggtctagagg ccgggtccgt ttctcgcctg gctggga
                                                                      37
<210> 36
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' PCR primer used to amplify EST R34808.
<400> 36
cacctgatcg cgagacccc
                                                                      19
<210> 37
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> Vector specific DNA sequencing primer (SP6).
<400> 37
gatttaggtg acactatag
                                                                      19
<210> 38
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Vector specific DNA sequencing primer (T7).
<400> 38
taatacgact cactataggg
                                                                      20
<210> 39
<211>
      22
<212> DNA
<213> Artificial Sequence
<220>
<223> Gene specific DNA sequencing primer.
<400> 39
ttacctgacc aaggaggagt gc
                                                                      22
```

```
<210> 40
<211>
      23
<212> DNA
<213> Artificial Sequence
<220>
<223> Gene specific DNA sequencing primer.
<400> 40
                                                                      23
aatccgctgc attcctgctg gtg
<210> 41
<211>
       20
<212> DNA
<213> Artificial Sequence
<220>
<223>
      Gene specific DNA sequencing primer.
<400> 41
cagtcactgg gccttgccgt
                                                                      20
<210> 42
<211> 105
<212>
      DNA
<213> Artificial Sequence
<220>
<223> 5' sense oligonucleotide used in Example 5.
<400> 42
gaaggggtaa gcttggataa aagatatgaa gaatactgca ccgccaacgc agtcactggg
                                                                     60
ccttgccgtg catccttccc acgctggtac tttgacgtgg agagg
                                                                     105
<210> 43
<211>
      129
<212> DNA
<213> Artificial Sequence
<220>
<223>
      3' antisense oligonucleotide used in Example 5.
<400> 43
cgcggatccc tactggcgga agcagcggag catgcaggcc tcctcagagc ggtagctgtt
                                                                     60
cttattgccc cggcagcctc catagatgaa gttattgcag gagttcctct ccacgtcaaa
                                                                    120
gtaccagcg
                                                                     129
<210> 44
```

<211> 207

```
<212> DNA
<213> Artificial Sequence
<220>
<223> Cloned bikunin fragment in Example 5.
<400> 44
gaaggggtaa gcttggataa aagatatgaa gaatactgca ccgccaacgc agtcactggg
                                                                       60
ccttgccgtg catccttccc acgctggtac tttgacgtgg agaggaactc ctgcaataac
                                                                      120
ttcatctatg gaggctgccg gggcaataag aacagctacc gctctgagga ggcctgcatg
                                                                      180
ctccgctgct tccgccagta gggatcc
                                                                      207
<210> 45
<211> 248
<212> PRT
<213> Artificial Sequence
<220>
<223>
      EST derived consensus sequence of human Bikunin (Figs. 4D and 4G).
<220>
<221>
      SIGNAL
<222>
      (1)..(23)
<223>
<400> 45
Met Leu Arg Ala Glu Ala Asp Gly Val Ser Arg Leu Leu Gly Ser Leu
Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp
            20
Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro
        35
                            40
                                                 45
Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr
    50
                        55
                                            60
Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys
65
                    70
                                        75
                                                             80
Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala
                85
                                    90
                                                         95
```

Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg

100 105 110

Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr 115 120 Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg 130 135 Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly 145 150 155 160 Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met 170 Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Leu Ala Gly Leu Phe Val Met Val Leu Ile Leu Phe 200 205 Leu Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln 210 215 220 Glu Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp Asp Lys Glu Gln 225 230 235

Leu Val Lys Asn Thr Tyr Val Leu 245

<210> 46

<211> 782

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (61)..(780)

<223>

<400> 46

acctgatege gagaceceaa eggetggtgg egtegeetge gegtetegge tgagetggee

108

60

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The second secon

atg gcg cag ctg tgc ggg ctg agg cgg agc cgg gcg ttt ctc gcc ctg Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu  $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15 \hspace{1.5cm}$ 

						tct Ser										156
						ctg Leu										204
						tgg Trp 55										252
						tgt Cys				_				_		300
_			_		_	aaa Lys	-	_		-				-	-	348
						agg Arg							-		_	396
						tct Ser										444
						gcc Ala 135							_	_	-	492
						ttt Phe										540
					Cys	cgg Arg	Gly	Asn	Lys	Asn						588
						tgc Cys										636
						gtg Val										684
						gcc Ala 215										732
cgg Arg 225	agg Arg	aac Asn	cag Gln	gag Glu	cgt Arg 230	gcc Ala	ctg Leu	cgc Arg	acc Thr	gtc Val 235	tgg Trp	agc Ser	ttc Phe	gga Gly	gat Asp 240	780
ga																782

<210> 47 <211> 240 <212> PRT <213> Homo sapiens <220> <221> SIGNAL <222> (1)..(27) <223> <400> 47 Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu Leu Gly Ser Leu Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg 40 45 Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln 50 55 Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr 70 75 Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr 85 90 Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser 100 Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn 115 120 Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala 130 135 140 Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn 145 150 155 Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu 165 170

who are the said of

Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Leu 180 Pro Leu Gly Ser Lys Val Val Leu Ala Gly Leu Phe Val Met Val 200 Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val Trp Ser Phe Gly Asp 230 235 <210> 48 <211> 1544 <212> DNA <213> Homo sapiens <220> <221> misc\_feature <222> (1358)..(1358) <223> "n" is any nucleotide. <220> <221> exon (301)..(1056) <222> <223> <400> 48 gcacgagttg ggaggtgtag cgcggctctg aacgcgctga gggccgttga gtgtcgcagg 60 cggcgagggc gcgagtgagg agcagaccca ggcatcgcgc gccgagaagg ccgggcgtcc 120 ccacactgaa ggtccggaaa ggcgacttcc gggggctttg gcacctggcg gaccctcccg 180 gagcgtcggc acctgaacgc gaggcgctcc attgcgcgtg cgcgttgagg ggcttcccgc 240 acctgatege gagaceceaa eggetggtgg egtegeetge gegtetegge tgagetggee 300 atg gcg cag ctg tgc ggg ctg agg cgg agc cgg gcg ttt ctc gcc ctg 348 Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu 10 ctg gga tcg ctg ctc ctc tct ggg gtc ctg gcg gcc gac cga gaa cgc 396 Leu Gly Ser Leu Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg 20 25 agc atc cac gac ttc tgc ctg gtg tcg aag gtg gtg ggc aga tgc cgg 444 Ser Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg 35 40 45

_		_				tgg Trp 55			_		_			_	5		492
						tgt Cys											540
_			-		_	aaa Lys	_	-		-				_	-		588
	_	_	_		-	agg Arg		-		-			_		-		636
						tct Ser											684
						gcc Ala 135											732
						ttt Phe											780
						cgg Arg			_		_		-				828
	-	-	_		_	tgc Cys		_	_	_					_		876
						gtg Val											924
						gcc Ala 215											972
			_		_	gcc Ala	_	_		_		_			_		1020
						aag Lys						tgad	eegee	cct			1066
gtc	gccaa	aga g	ggact	gggg	ga aç	ggag	ggga	a gad	ctato	gtgt	gago	ettt	tt t	caaat	agag	g	1126
gatt	gact	cg g	gattt	gagt	g at	catt	aggg	gctg	gaggt	ctg	tttc	ctctg	gg a	aggta	aggac	g	1186

<210> 49

<211> 252

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> (1)..(27)

<223>

<400> 49

Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu  $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$ 

Leu Gly Ser Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg 20 25 30

Ser Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg 35 40 45

Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln 50 55 60

Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr 65 70 75 80

Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr 85 90 95

Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser

Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn 115 120 125

Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala 135 140 Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn 150 155 Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Leu 185 Pro Leu Gly Ser Lys Val Val Leu Ala Gly Leu Phe Val Met Val 200 Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala 215 Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp 225 230 235 Asp Lys Glu Gln Leu Val Lys Asn Thr Tyr Val Leu 245 <210> 50 <211> 146 <212> PRT <213> Homo sapiens <400> 50 Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg 10 Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly 20 Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu 35

Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr

Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln

50

65					70					75					80
Asp	Ser	Glu	Asp	His 85	Ser	Ser	Asp	Met	Phe 90	Asn	Tyr	Glu	Glu	Tyr 95	Cys
Thr	Ala	Asn	Ala 100	Val	Thr	Gly	Pro	Cys 105	Arg	Ala	Ser	Phe	Pro 110	Arg	Trp
Tyr	Phe	Asp 115	Val	Glu	Arg	Asn	Ser 120	Суѕ	Asn	Asn	Phe	Ile 125	Tyr	Gly	Gly
Cys	Arg 130	Gly	Asn	Lys	Asn	Ser 135	Tyr	Arg	Ser	Glu	Glu 140	Ala	Суѕ	Met	Leu
Arg 145	Arg Cys 145														
<210 <211 <212 <213	> : > :	51 1530 ONA Artii	ficiá	al Se	equer	ıce									
<220 <223		Conse	ensus	s bil	cunir	ı seç	quenc	ce of	E Fig	g. 40	с.				
<220 <221 <222 <223	> r >	misc_ (46). "n" i	(46	5)	ıcled	otid∈	e.								
<220 <221 <222 <223	> r >	misc_ (117) "n" j	(1	17)	ıcled	otide	e.								
<220 <221 <222 <223	> I	(313)(313)													

<400> 51
gcgacctccg cgcgttggga ggtgtagcgc ggctctgaac gcgtgnaggg ccgttgagtg 60
tcgcaggcgg cgagggcgcg agtgaggagc agacccaggc atcgcgcgc gagaagncgg 120
gcgtccccac actgaaggtc cggaaaggcg acttccgggg gctttggcac ctggcggacc 180
ctcccggagc gtcggcacct gaacgcgagg cgctccattg cgcgtgcgtt tgaggggctt 240

cccgcacctg atcgcgagac cccaacggct ggtggcgtcg ctgcgcgtct cggctgagct 300 360 ggccatggcg cantgttgcg ggctgaggcg gacggcgttt ctcgcctgct gggatcgctg ctcctctctg gggtcctggc ggccgaccga gaacgcagca tccacgactt ctgcctggtg 420 tcgaaggtgg tgggcagatg ccgggcctcc atgcctaggt ggtggtacaa tgtcactgac 480 ggatcctgcc agctgtttgt gtatgggggc tgtgacggaa acagcaataa ttacctgacc 540 aaggaggagt gcctcaagaa atgtgccact gtcacagaga atgccacggg tgacctggcc 600 accagcagga atgcagcgga ttcctctgtc ccaagtgctc ccagaaggca ggattctgaa 660 gaccactcca gcgatatgtt caactatgaa gaatactgca ccgccaacgc agtcactggg 720 ccttgccgtg catccttccc acgctggtac tttgacgtgg agaggaactc ctgcaataac 780 ttcatctatg gaggctgccg gggcaataag aacagctacc gctctgagga ggcctgcatg 840 ctccgctgct tccgccagca ggagaatcct cccctgcccc ttggctcaaa ggtggtggtt 900 ctggcggggc tgttcgtgat ggtgttgatc ctcttcctgg gagcctccat ggtctacctg 960 atccgggtgg cacggaggaa ccaggagcgt gccctgcgca ccgtctggag ctccggagat 1020 gacaaggagc agctggtgaa gaacacatat gtcctgtgac cgccctgtcg ccaaqaggac 1080 tggggaaggg aggggagact atgtgtgagc tttttttaaa tagagggatt gactcggatt 1140 tgagtgatca ttagggctga ggtctgtttc tctgggaggt aggacggctg cttcctggtc 1200 tggcagggat gggtttgctt tggaaatcct ctaggaggct cctcctcgca tggcctgcag 1260 tctggcagca gccccgagtt gtttcctcgc tgatcgattt ctttcctcca ggtagagttt 1320 tctttgctta tgttgaattc cattgcctct tttctcatca cagaagtgat gttggaatcg 1380 tttcttttgt ttgtctgatt tatggttttt ttaagtataa acaaaagttt tttattagca 1440 ttctgaaaga aggaaagtaa aatgtacaag tttaataaaa aggggccttc ccctttagaa 1500 taaaaaaaaa aaaaaaaaaaaaaaaaaaaaaaa 1530

```
<210> 52
<211> 170
<212> PRT
```

Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val 1 5 10 15

<sup>&</sup>lt;213> Homo sapiens

<sup>&</sup>lt;400> 52

Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
20 25 30

Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser 35 40 45

Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val 50 60

Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp 65 70 75 80

Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser 85 90 95

Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr 100 105 110

Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg 115 120 125

Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn 130 135 140

Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln 145 150 155 160

Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys 165 170

<210> 53

<211> 27

<212> PRT

<213> Homo sapiens

<400> 53

Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu 1 5 10 15

Leu Gly Ser Leu Leu Ser Gly Val Leu Ala 20 25

<210> 54

<211> 23

```
<400> 54
Met Leu Arg Ala Glu Ala Asp Gly Val Ser Arg Leu Leu Gly Ser Leu
                                 10
Leu Leu Ser Gly Val Leu Ala
           20
<210> 55
<211>
     102
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' sense oligonucleotide used for construct #2 in Example 5.
<400> 55
60
tgtagagctt cttttccaag atggtacttt gatgttgaaa ga
                                                                102
<210> 56
<211> 129
<212> DNA
<213> Artificial Sequence
<220>
<223> 3' antisense oligonucleotide used for construct #2 in Example 5.
<400> 56
actggatcct cattggcgaa aacatctcaa catacaggct tcttcagatc tgtaagaatt
                                                                60
tttattacct ctacaaccac cgtaaataaa attattacaa gaatttcttt caacatcaaa
                                                                120
gtaccatct
                                                                129
<210> 57
<211> 108
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' sense oligonucleotide used for construct #3 in Example 5.
<400> 57
gaaggggtaa gcttggataa aagaaattac gaagaatact gtactgctaa tgctgttact
                                                                60
ggtccatgta gagcttcttt tccaagatgg tactttgatg ttgaaaga
                                                                108
```

<212> PRT

<213> Homo sapiens

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```
<210> 58
<211> 117
<212> DNA
<213> Artificial Sequence
<220>
<223>
      5' sense oligonucleotide used for construct #4 in Example 5.
<400> 58
gaaggggtaa gcttggataa aagagatatg tttaattacg aagaatactg tactgctaat
                                                                     60
gctgttactg gtccatgtag agcttctttt ccaagatggt actttgatgt tgaaaga
                                                                    117
<210> 59
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> Sense oligonucleotide used in PCR in Example 8.
<400> 59
cacctgatcg cgagacccc
                                                                      19
<210> 60
<211>
      23
<212> DNA
<213> Artificial Sequence
<220>
<223>
      Antisense oligonucleotide used in PCR in Example 8.
<400> 60
ctggcggaag cagcggagca tgc
                                                                      23
<210> 61
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide used in in vitro mutagenesis in Example 9.
<400> 61
cgcgtctcgg ctgacctggc cctgcagatg gcgcacgtgt gcggg
                                                                     45
<210> 62
<211> 60
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide used in in vitro mutagenesis in Example 9.
```

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```
<400> 62
ctgccccttg gctcaaagta ggaagatctt cccccgggg gggtggttct ggcggggctg
                                                                     60
<210> 63
<211> 14
<212> PRT
<213> Homo sapiens
<400> 63
Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Pro Leu Gly
                                   10
<210> 64
<211> 20
<212> PRT
<213> Homo sapiens
<400> 64
Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
                                   10
Val Gly Arg Cys
           20
<210> 65
<211> 20
<212> PRT
<213> Homo sapiens
<400> 65
Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys
                                   10
Arg Ala Ser Phe
           20
<210> 66
<211>
      11
<212>
      PRT
<213> Homo sapiens
<400> 66
Pro Arg Tyr Val Asp Gly Ser Gln Phe Tyr Gly
```

```
<210> 67
<211> 55
<212> PRT
<213> Homo sapiens
<400> 67
Val Val Leu Ala Gly Leu Phe Val Met Val Leu Ile Leu Phe Leu
                                   10
Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln Glu
           20
                               25
Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp Asp Lys Glu Gln Leu
Val Lys Asn Thr Tyr Val Leu
<210> 68
<211> 43
<212> PRT
<213> Homo sapiens
<400> 68
Val Val Leu Ala Gly Leu Phe Val Met Val Leu Ile Leu Phe Leu
                                   10
Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln Glu
           20
                               25
Arg Ala Leu Arg Thr Val Trp Ser Phe Gly Asp
<210> 69
<211> 55
<212> PRT
<213> Homo sapiens
<400> 69
Val Val Leu Ala Gly Leu Phe Val Met Val Leu Ile Leu Phe Leu
                                   10
```

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Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln Glu

25

Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp Asp Lys Glu Gln Leu  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Val Lys Asn Thr Tyr Val Leu 50 55

<210> 70

<211> 213

<212> PRT

<213> Homo sapiens

<400> 70

Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val

1 10 15

Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
20 25 30

Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser 35 40 45

Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val 50 55 60

Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp 65 70 75 80

Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser 85 90 95

Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr 100 105 110

Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg 115 120 125

Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn 130 135 140

Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln 145 150 155 160

Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
165 170 175

Leu Phe Val Met Val Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr 180 185 190

Leu Ile Arg Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val
195 200 205

Trp Ser Phe Gly Asp 210

<210> 71

<211> 225

<212> PRT

<213> Homo sapiens

<400> 71

Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val 1 5 10 15

Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr 20 25 30

Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser 35 40 45

Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val 50 55 60

Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp 65 70 75 80

Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser 85 90 95

Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr 100 105 110

Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg 115 120 125

Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn 130 135 140

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Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
145
                    150
                                        155
Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Leu Ala Gly
Leu Phe Val Met Val Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr
            180
                               185
Leu Ile Arg Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val
        195
                            200
                                                205
Trp Ser Ser Gly Asp Asp Lys Glu Gln Leu Val Lys Asn Thr Tyr Val
                        215
Leu
225
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<211> 19
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<213> Homo sapiens
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<223> "Xaa" is Ile, Thr, Asn, or Ser.
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Xaa Thr Xaa

<210> 73 <211> 108 <212> PRT <213> Homo sapiens

<400> 73

Pro Gly His Gln Gln Glu Cys Ser Gly Phe Leu Cys Pro Lys Ser Pro 1 5 10 15

POSSESSED STATES

Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr Glu 20 25 30

Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe 35 40 45

Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile 50 55 60

Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala 65 70 75 80

Cys Met Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Leu Pro Leu 85 90 95

Gly Ser Lys Val Val Leu Ala Gly Ala Val Ser 100 105

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<223> "Xaa" is Asp or Glu.

<400> 74

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1 5 10 15

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20 25 30
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                                                                       60
ccacgggtga cctggccacc agcaggaatg cagcggattc ctctgtccca agtgctccca
                                                                      120
gaaggcagga ttctgaagac cactccagcg atatgttcaa ctatgaagaa tactgcaccg
                                                                      180
ccaacgcagt cactgggcct tgccgtgcat ccttcccacg ctggtacttt gacgtggaga
                                                                      240
ggaactcctg caataacttc atctatggag gctgccgggg caataagaac agctaccgct
                                                                      300
ctgaggaggc ctgcatgctc cgctgcttcc gccagcagga gaatcctccc ctgccccttg
                                                                      360
gctcaaaggt ggtggttctg gccggggctg tttcgtgatg gtgttgatcc ttttcctggg
                                                                      420
gagcntccat ggtcttactg attccgggtg gcaaggagga accaggagcg tgccctgcgg
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ancgtctgga gcttcggaga tgacaagggn t
                                                                      511
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<211>

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31

PRT

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Glu Glu Pro Gly Ala Cys Pro Ala Xaa Arg Leu Glu Leu Arg Arg
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gcgacctccg cgcgttggga ggtgtagcgc ggctctgaac gcgtngagng gccgttgagt
                                                                     60
gtcgcaggcg gcgagggcgc gagtgaggag cagacccagg catcgcgcgc cgagaagncg
```

ALC DE TOTAL DE LA CONTRACTION DE LA CONTRACTION

Meant

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ggcgtcccca cactgaaggt ccggaaaggc gacttccggg ggctttggca cctggcggac
                                                                     180
cctcccggag cgtcggcacc tgaacgcgag gcgctccatt gcgcgtgcgt ntgaggggct
                                                                     240
tecegeaect gategegaga ecceaaegge tggtggegte geetgegegt eteggetgag
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ctggncatgt cg
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tegeaggegg egagggegeg agtgaggage agacceagge ategegegee gagaagnegg
                                                                     120
gcntccccac actgaaggtc cggaaaggcg acttccgggg gctttggcac ctggcggacc
                                                                     180
ctcccggagc gtggcacctg aacgcgaggc gctccattgc gcgtgcgttt gaggggcttc
                                                                     240
ccgcacctga tcgcgagacc ccaacggctg gtggcgtcgc ctgcgcgtct cggctgagct
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ggccatggcg cactgtgcgg ngctgaggcg
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CANAL CONTRACTOR SAN LINES

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aaggccgggc gtccccacac tgaaggtccg gaaaggcgac ttccgggggc tttggcacct
                                                                    120
ggcggaccet cccggagcgt cggcacctga acgcgaggcg ctccattgcg cgtgcgtttg
                                                                    180
aggggettee egeacetgat egegagaeee caaeggetgg tngegteget negegteteg
                                                                    240
gctgagcttg gccatggcgc antgttncgg gctnaggcgg acg
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cgcaggcggc agggcngagt gaggagcaga cccaggcatc gcgcgccgag aagncgggcg
                                                                    120
tccccacact gaaggtccgg aaaggcgact tccgggggct ttggcacctg gcggacgtcc
                                                                    180
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cggagcnggc acctgaacgc gaggcgctcc attgcgcgtg cgtttgaggg gcttcccgca
                                                                    240
cctgatcgcg agaccccaac ggctggtngc gtcgctggcg cgttctcggc tgagctggcc
                                                                     300
atggcgcant gttgcgngct gaggcggacc gncgtttttc ttcgccttgc tgggattcgc
                                                                    360
ttgcttcctn tctgggggtt cctgggcggc cgaccgagaa cgcagcatcc aagaattttt
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gcc
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gaaaggcgac ttccgggggc tttggcacct ggcggaccct cccggagcgt cggcacctga
                                                                     120
acgcgaggcg ctccattgcg cgtgcgtntg gaggggcttc ccgcacctga tcgcgagacc
                                                                     180
ccaacggctg gtgggcgtcg ctgcgcgtct tcggctgagc tgggccatgg cgcanttgtt
                                                                     240
gegggetgag geggaegegg negtttttte gneettgetg ggattegttg tinetetetn
ggggttctgg ggnggccgan cgagaacgca agcattcacg attt
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gcttcccgca cctgatcgcg agaccccaac ggctggtggc gtcgctgcgc gtctcggctg
                                                                      120
agctggccat ggcgcantgt tgcgngctga ggcggcggnc gttttctcgc ctgctgggat
                                                                      180
cgctgctcct ctctggggtc ctggcggccg accgagaacg cagcatccac ganttcttcc
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                                                                      253
tggtgttcga agg
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tgaggagcag acccaggcat cgcgcgccga gaagncgggc gtccccacac tgaaggtccg
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gaaaggcgac ttccgggggc tttggcacct ggcggaccct cccggagcgt cggcacctga
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acgcgaggcg ctccattgcg cgtgcgtttg aggggcttcc cgcacctgat cgcgagaccc
                                                                     240
caacggctgg tggcgtcgcc tgcgcgtctc ggctgagctg gccatggcgc antggtgcgg
                                                                    300
gcttgaggcg gannngccgt ttctcgcctg ctgggatcgc tgctcctctc tggggtcctg
                                                                     360
gcggccgacc gagaacgcag catccacgac ttctgcctgg tgtcgaaggt ggtgggcag
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acttccgggg gctttggcac ctggcggacc ctcccggagc gtcggcacct gaacgcgagg
                                                                     120
cctccattgc cgtgcgttng aggggcttcc cggaacttga tcgcgagacc ccaacggctg
                                                                     180
gtggcgtcgc tgcgcgtcct cggctgagct ggccatggcg cantggtgcc gngctgaggc
                                                                     240
cggagggccg gtttctcgcc ttgctgggat cgctgctcct ctctggggtc ctggcggccg
                                                                     300
ancgaagaan gcagcaatcc angaattnct gcctggtgtt cgaaagttgg tgggcanatt
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ccggggcctt catgnctaag gttggttggt anaatgtnaa ttaangattc ttgcaactgt
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ttgtgtnatt ggggctntta aacggaaana caataatnac ctgaccaaag aagnaat
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accgagaacg cagcatccac gacttctgcc tggtgtcgaa ggtggtgggc agattccggg
                                                                     120
cctccatgcc taggtggtgg tacaatgtca ctgacggatc ctgccagctg tttgtgtatg
                                                                     180
ggggctgtga cggaaacagc aataattacc tgaccaagga ggagtgcctc aagaaatgtg
                                                                     240
ccactgtcac agagaatgcc acgggtgacc tggccaccag caggaatgca gcggattcct
                                                                     300
ctgtcccaag tgctcccaga aggcaggatt cttgaagacc acttcagcga tatgtttcaa
                                                                     360
ntattgnaag aataattgca ccgncaacgn att
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agaacgcagc atccacgact tctgcctggt gtcgaaggtg gtgggcagat gccgggcctc
                                                                     120
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catgcctagg tggtggtaca atgtcactga cggatcctgc cagctgtttg tgtatggggg
                                                                     180
ctgtgacgga aacagcaata attacctgac caaggaggag tgcctcaaga aatgtgccac
                                                                     240
tgtcacagag aatgccacgg gtgacctggc caccagcagg aatgcagcgg attcctctgt
                                                                     300
cccaagtgct cccagaaggc aggattctga agaccactcc agcgatatgt tcaactatga
                                                                     360
agaatactgg caccgccaac gcattcactg ggcctgcgtg catccttccc acgctggtac
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tttgncgt
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cttctgcctg gtgtcgaagg tggtgggcag atgccgggcc tccatgccta ggtggtggta
                                                                     120
caatgtcact gacggatcct gccagctgtt tgtgtatggg ggctgtgacg gaaacagcaa
                                                                     180
taattacctg accaaggagg agtgcctcaa gaaatgtgcc actgtcacag agaatgccac
                                                                     240
gggtgacctg gccaccagca ggaatgcagc ggattcctct gtcccaagtg ctcccagaag
                                                                     300
gcaggattct gaagaccact ccagcgatat gttcaactat gaagaatact gcaccgccaa
                                                                     360
cgcagtcact ggggccttgc gtggaatcct ttcccacgct ggnaatttng acgttgagaa
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ggaac
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      88
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tnccactgtc acagagaatg ccacgggtga cctggccacc agcaggaatg cagcggattc
                                                                     120
ctctgtccca agtgctccca gaaggcagga ttctgaagac cactccagcg atatgttcaa
                                                                     180
ctatgaagaa tactgcaccg ccaacgcagt ncactgggcc ttgcgtggca tnccttccca
                                                                     240
cgctngtact ttgacgtgga gaggaactcc tggcaataac ttcatctatg gaggcttgcc
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ggggcaatna agaacagntt accgctcttt aggaggcctg cat
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aaggcaggat totgaagaco actocagoga tatgttcaac tatgaagaat actgcacogo
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caacgcagtc actgggcctt gccgtgcatc cttcccacgc tggtactttg acgtggagag
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gaactcctgc aataacttca tctatggagg ctgccggggc aataagaaca gctaccgctc
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tgaggaggcc tgcatgctcc gctgcttccg ccagcaggag aatcctcccc tgccccttgg
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ctcaaaggtg gtggttctgg ccggggctgt ttcgtgatgg tgttgatcct tttcctgggg
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ccctgcgcac cgtctgggag ctccggagat gacaagggag cagctgggtg aagaacacat
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gacaaggagc agctggtgaa gaacacatat gtcctgtgac cgccctgtcg ccaagaggac
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cagggagcgt gccctgcgna ccgtctngga gctccggaga tgacaaggag cagctggtga
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tggcggggct gttcgtgatg gtgttgatcc tcttcctggg agcctccatg gtctacctga
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                                                                     240
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tgacaaggga gcagctggtg aagaacacat atgttcctgt tgaccgccct gttcgccaag
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gagctccgga gatgacaagg agcagctggt gaagaacaca tatgtcctgt gaccgccctg
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tcgccaagag gactggggaa gggaggggag actatgtgtg agctttttt aaatagaggg
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gaaggaaagt aaaatgtaca agtttaataa a

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						ttttaagta		240
						aagtttaata		300
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		cca	guutuaaaaa	uuuuuaaaaa	uuuuaaaaad	uaa		J43